This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. – 5 (Cancelled)

6. (Currently amended) The method of claim 26, wherein step c) of utilizing the calculated dimensions, chemical and/or electrostatic properties obtained in step b) to identify ~~small molecule~~ compounds that contain at least one functional group that can be accommodated by said cavity comprises utilizing the calculated dimensions, chemical and or electrostatic properties obtained step b) to identify ~~small molecule~~ compounds comprising at least one functional group having shape complementarity to said cavity.

7. (Currently amended) The method of claim 26, wherein step d) of assaying said ~~small molecule~~ compounds in vitro to identify a ~~small molecule~~ compound which binds within said cavity and modulates intermolecular interaction at the functionally critical site between said target protein and said proteinaceous modifier comprises assaying said ~~small molecule~~ compounds in vitro to identify a ~~small molecule~~ compound that inhibits intermolecular interactions between said target protein and said proteinaceous modifier.

8. (Currently amended) The method of claim 26, wherein step d) of assaying said ~~small molecule~~ compounds in vitro to identify a ~~small molecule~~ compound which binds within said cavity and modulates intermolecular interaction at the functionally critical site between said target protein and said proteinaceous modifier comprises assaying said ~~small molecule~~ compounds in vitro to identify a ~~small molecule~~ compound that enhances intermolecular interactions between said target protein and said proteinaceous modifier.

9. (Canceled)

10. (Withdrawn) The method of claim 9, wherein the target protein is a receptor.

11. (Withdrawn) The method of claim 9, wherein the receptor is a member of the TNF receptor superfamily.

12. (Withdrawn) The method of claim 11, wherein the TNF receptor superfamily member is selected from the group consisting of the TNF receptor, fas, CD40, gp120, fas ligand, TNF-α, ß-latamese, c-erbB2, growth hormone receptor, growth hormone, insulin receptor, insulin, IL-1 receptor, IL-1, IL-2 receptor, IL-2, epidermal growth factor receptor (EGFR), and epidermal growth factor.

13. (Withdrawn) The method of claim 12, wherein the TNF receptor superfamily member is a TNF receptor.

14. (Canceled)

15. (Canceled)

16. (Withdrawn) The method of claim 9, wherein the target protein is a member of the immunoglobulin superfamily.

17. (Withdrawn) The method of claim 16, wherein the target protein is CD4.

18. (Canceled)

19. (Withdrawn/Currently amended) The method of claim 18, wherein the modifier is a protein selected from the group consisting of a membrane-bound protein, a cytosolic protein, a nuclear protein, ~~an enzyme substrate,~~ a cytokine, a lymphokine, a chemokine, an adhesion molecule, a growth factor, or a receptor thereof.

20. (Withdrawn) The method of claim 18, wherein the modifier is a member of the TNF receptor family.

21. (Withdrawn/Currently amended) The method of claim 18, wherein the modifier is selected from the group consisting of TNF receptor, fas, CD40, gp120, fas ligand, TNF- α, ~~β-lactam, c-~~erbB2, growth hormone receptor, growth hormone, insulin receptor, insulin, IL-1 receptor, IL-1, IL-2 receptor, IL-2, epidermal growth factor receptor (EGFR), MHC/antigen/TCR complex, and epidermal growth factor.

22. (Withdrawn) The method of claim 21, wherein the modifier is TNF- α.

23. (Canceled)

24. (Withdrawn) The method of claim 19, wherein the modifier is the MHC/antigen/TCR complex.

25. (Previously presented) The method of any one of claims 26, 28, 29 or 30, wherein identifying the cavity within the structure of a target protein in step a) comprises using nuclear magnetic resonance, crystal structure analysis, calorimetric values from thermodynamic studies, or computer modeling.

26. (Currently amended) A method of identifying a ~~small molecule~~ compound that is an allosteric modulator of an intermolecular interaction between a target protein and a proteinaceous modifier at a functionally critical site of [[a]] said target protein ~~and a modifier~~, which comprises:

a) identifying an allosteric cavity on [[a]] the target protein that is within about 15 to 20 angstroms of said functionally critical site on the target protein, wherein said target protein is a

membrane-bound protein, a cytosolic protein, a nuclear protein, a cytokine, a lymphokine, a chemokine, an adhesion molecule, a growth factor, or a receptor thereof;

b) calculating the dimensions of said cavity and mapping the chemical and/or electrostatic properties of said cavity;

c) utilizing the calculated dimensions, chemical and/or electrostatic properties obtained in step b) to identify ~~small molecule~~ compounds that contain at least one functional group that can be accommodated by said cavity;

d) testing said ~~small molecule~~ compounds in an in vitro assay to detect a ~~small molecule~~ compound which modulates the interaction at the functionally critical site between said target protein and said proteinaceous modifier;

thereby identifying said ~~small molecule~~ compound that is an allosteric modulator of [[an]] said intermolecular interaction at said functionally critical site ~~between said target protein and said modifier~~.

27. (Canceled)

28. (Currently amended) A method of identifying a ~~small molecule~~ compound that is an allosteric modulator of an intermolecular interaction associated with a predetermined biological function to be modulated, said interaction occurring between a target protein and a proteinaceous modifier at a functionally critical site on a target protein, which method comprises:

a) identifying an allosteric cavity that is within about 15 to 20 angstroms on the target protein from the functionally critical site, wherein said target protein is a membrane-bound protein, a cytosolic protein, a nuclear protein, a cytokine, a lymphokine, a chemokine, an adhesion molecule, a growth factor, or a receptor thereof;

b) calculating the dimensions of said cavity;

c) mapping the chemical and/or electrostatic properties of said cavity;

d) utilizing the calculated dimensions of step b) or the chemical and/or electrostatic properties obtained in step c) to identify ~~small molecule~~ compounds that contain at least one functional group that can be accommodated by said cavity;

e) testing said ~~small molecule~~ compounds in an in vitro assay to detect a ~~small molecule~~ compound which modulate the interaction at the functionally critical site between said target protein and said modifier;

thereby identifying said ~~small molecule~~ compound that is an allosteric modulator of the intermolecular interaction at said functionally critical site between said target protein and said proteinaceous modifier.

29. (Currently amended) A method of identifying a ~~small molecule~~ compound that is an allosteric modulator of an intermolecular interaction at a functionally critical site on a target protein, wherein the intermolecular interaction at a functionally critical site is between the target protein and a proteinaceous modifier, and wherein the interaction is associated with a predetermined biological function to be modulated, which method comprises:

a) identifying an allosteric cavity that is within about 15 to 20 angstroms of the functionally critical site on the target protein, wherein said target protein is a membrane-bound protein, a cytosolic protein, a nuclear protein, a cytokine, a lymphokine, a chemokine, an adhesion molecule, a growth factor, or a receptor thereof;

b) calculating the dimensions of said cavity and mapping the chemical and/or electrostatic properties of said cavity;

c) utilizing the calculated dimensions, chemical and/or electrostatic properties obtained in step b) to identify ~~small molecule~~ compounds that contain at least one functional group that can be accommodated by said cavity;

d) testing said ~~small molecule~~ compounds in an in vitro assay to detect a ~~small molecule~~ compound which modulates the interaction at the functionally critical site between said target protein and said proteinaceous modifier;

thereby identifying said ~~small molecule~~ compound that is an allosteric modulator of the interaction at the functionally critical site between said target protein and said proteinaceous modifier.

30. (Currently amended) A method of identifying a ~~small molecule~~ compound that is an allosteric modulator of an intermolecular interaction at a functionally critical site, wherein the functionally critical site is the site of the intermolecular interaction between a target protein and a proteinaceous modifier that is necessary for the specific biological function attributed to the target protein, which method comprises the steps of

a) identifying an allosteric cavity that is within about 15 to 20 angstroms of the functionally critical site on the target protein, wherein said target protein is a membrane-bound protein, a cytosolic protein, a nuclear protein, a cytokine, a lymphokine, a chemokine, an adhesion molecule, a growth factor, or a receptor thereof;

b) calculating the dimensions of said cavity and mapping the chemical and/or electrostatic properties of said cavity;

c) utilizing the calculated dimensions, chemical and/or electrostatic properties obtained in step b) to identify ~~small molecule~~ compounds that contain at least one functional group that can be accommodated by said cavity;

d) testing said ~~small molecule~~ compounds in an in vitro assay to detect a ~~small molecule~~ compound which modulates the interaction at the functionally critical site between said target protein and said proteinaceous modifier;

thereby identifying said ~~small molecule~~ compound that is an allosteric modulator of the interaction at the functionally critical site between said target protein and said proteinaceous modifier.

31. (Previously Presented) The method of claim 25, wherein the allosteric cavity is identified using nuclear magnetic resonance or crystal structure analysis, and further comprises identifying thermal β-factors.

32. (Withdrawn) The method of claim 13 wherein the modifier is TNF-α.